typhus. The complete genome sequence of OT have recently been determined. However, the early signaling events involved in the entry of OT into mammalian cells remain a challenge. In this study, we have demonstrated that adherence ability and comparison of three major outer membrane protein TSA56 (includes TSA56-antigen domain I and TSA56-antigen domain III), TSA47 and TSA22 of OT.
Methods: After expression and purification of three major outer membrane proteins TSA56, TSA47 and TSA22 of OT in *E. coli*, the proteins were examined for reactivity and antiserum titer with 22 OT-infected patients' antiserum by immunoblot assay. In vitro adhesion assay was performed to determine the adherence ability of different bacterial outer membrane proteins on the host cells by overexpression outer membrane protein of OT in *E. coli*.
Results: The antiserum titer against three major outer membrane proteins of OT was markedly higher in TSA56 compared to TSA47 and TSA22. In adhesion assay, adhesion of host cells with TSA56-expressed *E. coli* was significantly increased than TSA47 and TSA22. Furthermore, adhesion experimant and antiserum titer against antigen-domain I (ADI) region (19–114aa) in the extracellular domain of TSA56 were also dramatically higher than previously reported antigen-domain III (ADIII) region (237–366aa).
Conclusion: Taken together, our data clearly indicated that OT exploits TSA56-mediated bacterial adhesion, abundant antiserum titer and ADI region of TSA56 may draw another adhesion site (except for ADIII) to invade eukaryotic host cells.

OL-063 Antibiotic susceptibility of *Serratia* spp. isolated from hospitalised patients in a general hospital

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Aim: to evaluate the antimicrobial susceptibility of clinical isolates of *Serratia spp*. over a 7-year period.
Materials and Methods: A total of 43 *Serratia spp.* isolated from symptomatic patients in our hospital, were studied. Samples were cultured on appropriate media. The blood cultures were incubated in Bactec 9120 system (Becton Dickinson®) in aerobic plus, anaerobic plus and mycosis vials. All the positive cultures were Gram strained and re-cultured in blood agar, Mac Conkey agar, Sabouraud with TCC and Chromagarcandida (Becton Dickinson®). The identification of the isolates and the susceptibility testing were performed by the VITEK system (bioMerieux®, Marcyl'Etolie, France) and susceptibility disc diffusion method according to Clinical Laboratory Standards Institute (CLSI) guidelines.
Results: They were recorded in 2002 1 executive, in 2003 3, in 2004 6, in 2005 8, in 2006 8, in 2007 8 and in 2008 9. Were isolated 22 executives from men and 21 from women. The identification of executives showed 9 S. *liquefaciens*, 7 S. *fonticola*, 23 S. *marcescens*, 2 S. *odorifera*, 1 S. *rubidaea* and 1 S. *plymuthica.* We isolated 9 from bronchial excretions, 19 from blood and 15 from urine. In the 95% of cases existed the conditions that encourage the growth of inflamation. The executives *Serratia spp* presented high resistance in ampicillin, amoxicillin/clavulanate, mediocre resistance in tombramycin and low resistance in amikacin, gentamycin, ceftazidime. Sensitivity 100% they presented the all executives in trimethoprimi/sulfomethoxazoli, ciprofloxacin and imipenem.
Conclusions: The blood, the urine and the bronchial excretions were the mainer sources of isolation of executives. Exist increased need of recovery of source of origin of microbes, application of metres of control of infections and continuous recording of resistance of executives for the better protection of sicks.

OL-064 Superantigen gene profiles and presence of exfoliative toxin genes in community-acquired meticillin-resistant *Staphylococcus aureus* isolated from Chinese children

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Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) has emerged as a significant pathogen in the community. It is proposed that the simultaneous assessment of virulence gene profiles and genetic background increases the discriminatory power of genetic investigations into the mechanisms of *S. aureus* pathogenesis. *S. aureus* strains harbour staphylococcal superantigen (SAg) genes, and most are encoded by mobile genetic elements (MGEs).
Methods: Ninety-nine CA-MRSA strains were isolated from eight hospitals in China from July 2008 to June 2009. Multilocus sequence typing (MLST) were performed. Each isolate was tested by six multiplex PCRs for the toxin genes.
Results: Of the CA-MRSA isolates, 88.9% (88/99) harboured toxin genes, with *sek* as the most frequent toxin gene (62.6%), followed by *seq* (61.6%), *seb* (60.6%) and *sea* (35.4%). The *eta* gene was detected only in one ST398-IVa-*spa* t034 strain. The *sed* and *etd* genes were not found in any of the isolates tested. A total of 38 virulence genotypes were observed, of which the genotype *seb-sek-seq* (27.3%, 24/88) comprised the majority, followed by *sea-seb-sek-seq* (18.2%, 16/88). The enterotoxin gene cluster including *seg-sei-sem-sen-seo-seu* predominated at a rate of 15.1%. The relationship among toxin genotypes, toxin genes encoding profiles of mobile genetic elements and genetic background was analysed. Among 66 clonal complex (CC) 59 isolates, 87.9% (58/66) were positive for toxin genes, and 75.8% (50/66) harboured the toxin gene combination *seb-sek-seq*. Among *seb-sek-seq*-positive CC59 strains, 42.0% (21/50) also carried the *sea* gene. CC59 corresponded exclusively to *agr*-1.
Conclusions: The distribution of toxin genes was closely linked to the genetic background (CC) of the strain. Some gene combinations suggested the possibility of the existence of variants or new types of MGE.

Free Paper Presentation 9: HIV/AIDS
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PL-009 Patterns of decrease in CD4 cell count after seroconversion: comparison between Beijing PRIMO cohort and CASCADE seroconverter cohorts

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Background: The HIV epidemic among men who have sex with men (MSM) in Beijing is of increasing concern. To date, differences in rate of progression to AIDS or of CD4 cell loss have emerged regarding subtype D although comparisons have been restricted to western and Africans countries. We estimate the rate of CD4 loss following seroconversion from MSM in China and in resource-rich countries.